

GenCore version 5.1.9
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OM nucleic - nucleic search, using sw model

Run on: December 14, 2006, 13:20:45 ; Search time 16567.7 Seconds
(without alignments)
10189.779 Million cell updates/sec

Title: US-10-767-441-9
Perfect score: 2640
Sequence: 1 taaacggcgataataaata.....acaggattaattcccgacc 2640

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues
Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb env.*
- 2: gb pat.*
- 3: gb ph.*
- 4: gb pl.*
- 5: gb pr.*
- 6: gb ro.*
- 7: gb sts.*
- 8: gb sy.*
- 9: gb un.*
- 10: gb vi.*
- 11: gb ov.*
- 12: gb htg.*
- 13: gb in.*
- 14: gb om.*
- 15: gb ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2640	100.0	225528	15	AL591984 Listeria
2	2640	100.0	244528	2	AX641673 Sequence
3	2556	96.8	2556	2	AX413703 Sequence
4	2556	96.8	2556	2	AX415879 Sequence
5	2197.6	83.2	105187	15	Continuation (29 of
C 6	977.4	37.0	3318	2	AX416769 Sequence
7	676.2	25.6	759	2	AX415918 Sequence
C 8	530.4	20.1	3084	2	AX416693 Sequence
9	269.2	10.2	110000	15	AX414526 Sequence
10	269.2	10.2	110000	15	Continuation (9 of
C 11	232	8.8	260050	15	AL596166 Listeria
C 12	232	8.8	349980	2	AX417039 Sequence
C 13	232	8.8	349980	2	AX417042 Sequence
14	231	8.8	1941	2	AX413668 Sequence
15	231	8.8	1974	2	AX415259 Sequence
16	224	8.5	3714	2	AX415307 Sequence
17	224	8.5	3735	2	AX413690 Sequence
18	224	8.5	263020	2	AX417040 Sequence

19	224	8.5	333050	15	AL596168 Listeria
20	224	8.5	349980	2	AX417043 Sequence
21	224	8.5	349980	2	AX417044 Sequence
22	216	8.2	110000	15	Continuation (13 of
23	204.2	7.7	2823	2	AX415054 Sequence
24	204.2	7.7	324050	15	AL591983 Listeria
25	204.2	7.7	349980	2	AX641672 Sequence
26	202.8	7.7	110000	15	Continuation (25 of
C 27	199.8	7.6	224650	15	AL596164 Listeria
C 28	199.8	7.6	349980	2	AX417041 Sequence
C 29	199.8	7.6	349980	2	AX453571 Sequence
30	191.6	7.3	248050	15	AL596172 Listeria
31	191.6	7.3	349980	2	AX413018 Sequence
32	191.6	7.3	349980	2	AX417048 Sequence
C 33	188	7.1	160050	15	AL591974 Listeria
C 34	188	7.1	349980	2	AX641665 Sequence
C 35	186.8	7.1	2977	2	AX416727 Sequence
C 36	185	7.0	849	2	AX416268 Sequence
C 37	183.2	6.9	110000	15	Continuation (4 of
C 38	177.4	6.7	1018	2	AX416178 Sequence
C 39	176.8	6.7	753	2	AX414618 Sequence
C 40	146.2	5.5	744	2	AX416997 Sequence
C 41	145.2	5.5	1704	2	AX416578 Sequence
C 42	140.2	5.3	895	2	AX414851 Sequence
43	138	5.2	1320	2	AX413786 Sequence
44	138	5.2	1320	2	AX415814 Sequence
C 45	138	5.2	240050	15	AL591979 Listeria

ALIGNMENTS

RESULT 1
AL591984
LOCUS
DEFINITION
AL591984 Listeria monocytogenes strain EGD, complete genome, segment 12/12.
ACCESSION
AL591984.1 GI:16412145
VERSION
KEYWORDS
SOURCE
Listeria monocytogenes
ORGANISM
Listeria monocytogenes
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE
1.
AUTHORS
Glaser, P., Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A., Baquero, F., Berche, P., Bloeker, H., Brandt, P., Chakraborty, T., Charbit, A., Chetoui, F., Couve, E., de Daruvar, A., Dehoux, P., Domann, S., Dominguez-Bernal, G., Duchaud, E., Durant, L., Dussurgeat, O., Entian, K.D., Fsihi, H., Garcia-del Portillo, F., Garrido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T., Hauf, J., Jackson, D., Jones, L.M., Kaerst, U., Kref, J., Kuhn, M., Kunst, F., Kurapkat, G., Madueno, E., Maitournam, A., Vicente, J.M., Ng, E., Nedjari, H., Nordstiek, G., Novella, S., de Pablo, B., Perez-Diaz, J.C., Purcell, R., Rammel, B., Rose, M., Schluter, T., Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and Cossart, P.

AL591984 225528 bp DNA linear BCT 16-APR-2005
Listeria monocytogenes strain EGD, complete genome, segment 12/12.
AL591984.1 GI:16412145
Listeria monocytogenes
Listeria monocytogenes
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
1.
Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A., Baquero, F., Berche, P., Bloeker, H., Brandt, P., Chakraborty, T., Charbit, A., Chetoui, F., Couve, E., de Daruvar, A., Dehoux, P., Domann, S., Dominguez-Bernal, G., Duchaud, E., Durant, L., Dussurgeat, O., Entian, K.D., Fsihi, H., Garcia-del Portillo, F., Garrido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T., Hauf, J., Jackson, D., Jones, L.M., Kaerst, U., Kref, J., Kuhn, M., Kunst, F., Kurapkat, G., Madueno, E., Maitournam, A., Vicente, J.M., Ng, E., Nedjari, H., Nordstiek, G., Novella, S., de Pablo, B., Perez-Diaz, J.C., Purcell, R., Rammel, B., Rose, M., Schluter, T., Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and Cossart, P.

Comparative genomics of Listeria species
Science 294 (5543), 849-852 (2001)
11679669
2 (bases 1 to 225528)
Frangeul, L., Frangeul, L. and Rusniok, C.
Direct Submission
Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris
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E-mail: pglaser@pasteur.fr
Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.
Location/Qualifiers
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/strain="EGD-e"
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complement(56..775)

COMMENT
FEATURES
source
gene

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DEFINITION Sequence 2863 from Patent WO010118.
ACCESSION AX641673
VERSION AX641673.1 GI:28474434
KEYWORDS Listeria monocytogenes
SOURCE Listeria monocytogenes
ORGANISM Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
REFERENCE 1
AUTHORS Buchrieser,C., Frangeul,L., Couve,E., Rusniok,C., Pshhi,H., Dehoux,P., Dussurget,O., Chetouani,F., Nedjari,H., Glaser,P., Kunst,F., Cossart,P., Daniels,J., Goebel,W., Krefte,J., Kuhn,M., Ng,E., Vasquez-Boland,J., Dominguez-Bernal,G., Garrido-Garcia,P., Tierrez-Martinez,A., Amend,A., Chakraborty,T., Domann,E., Hain,T., Berche,P., Charbit,A., Durant,L., Perez-Diaz,J.C., Baquero,F., Garcia del Portillo,F., Gomez-Lopez,N., Madueno,E., de Fabios,B., Wehland,J., Kaerst,U., Entian,K.D., Hauf,J., Rose,M. and Voss,H.
TITLE Listeria monocytogenes genome, polypeptides and uses
JOURNAL Patent: WO 010118-A 2863 11-APR-2001;
INSTITUT PASTEUR (FR)

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ACCESSION AX415879
VERSION AX415879.1 GI:21448336
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SOURCE Listeria monocytogenes EGD-e
ORGANISM Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
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1 Kunst, F. and Glaser, P.
AUTHORS Listeria inocua, genome and applications
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JOURNAL INSTITUT PASTEUR (FR); CENTRE NATIONAL DE LA RECHERCHE
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QY 2153 ACTTTTACCACAGGACGCAAAACCGGTACATATGTGTATATTAATAAACAATCGAAGCAGCA 2212
Db 2101 ACTTTTACCACAGGACGCAAAACCGGTACATATGTGTATATTAATAAACAATCGAAGCAGCA 2160
QY 2213 GAGCGATAACAGTGAATTTACGTGGATGTGATGCGAACAACCTCGCTCCATCCGAACA 2272
Db 2161 GAGCGATAACAGTGAATTTACGTGGATGTGATGCGAACAACCTCGCTCCATCCGAACA 2220
QY 2273 TTTAAACGAAAACGTTGGCGACACATATAAGCAACTGCGCAAAACAAATCGACGGCTACACA 2332
Db 2221 TTTAAACGAAAACGTTGGCGACACATATAAGCAACTGCGCAAAACAAATCGACGGCTACACA 2280
QY 2333 TTATCGCGCAACCAACCAATGCGACTGGACAAATTTCAAAAGTAGCGGCAAAATCTGTCAAC 2392
Db 2281 TTATCGCGCAACCAACCAATGCGACTGGACAAATTTCAAAAGTAGCGGCAAAATCTGTCAAC 2340
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QY 2393 TACATTTATACGAAAAACACAAACACAGATCAACCTTTTACCAACTTAAAAAACCTTACGAAC 2452
Db 2341 TACATTTATACGAAAAACACAAACACAGATCAACCTTTTACCAACTTAAAAAACCTTACGAAC 2400
QY 2453 ACCACACAAACCAAGCCATCTAATTTAAAGCAACCGAAGTGAAAAAGCTTTCAGATACC 2512
Db 2401 ACCACACAAACCAAGCCATCTAATTTAAAGCAACCGAAGTGAAAAAGCTTTCAGATACC 2460
QY 2513 CTACAAAAACAGCGGATTCGACACCATGGAATCAGCTCTACTTGGGGTATTCCTATCA 2572
Db 2461 CTACAAAAACAGCGGATTCGACACCATGGAATCAGCTCTACTTGGGGTATTCCTATCA 2520
QY 2573 TCCACAGCTCTAGTTATCTCGAAAAAGAAAAAATAG 2608
Db 2521 TCCACAGCTCTAGTTATCTCGAAAAAGAAAAAATAG 2556
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RESULT 5

AE017262_28

WPCOMMENT

Sequence split into 29 fragments LOCUS AE017262 Accession AE017262

Fragment Name	Begin	End
AE017262_00	1	110000
AE017262_01	100001	210000
AE017262_02	200001	310000
AE017262_03	300001	410000
AE017262_04	400001	510000
AE017262_05	500001	610000
AE017262_06	600001	710000
AE017262_07	700001	810000
AE017262_08	800001	910000
AE017262_09	900001	1010000
AE017262_10	1000001	1110000
AE017262_11	1100001	1210000
AE017262_12	1200001	1310000
AE017262_13	1300001	1410000
AE017262_14	1400001	1510000
AE017262_15	1500001	1610000
AE017262_16	1600001	1710000
AE017262_17	1700001	1810000
AE017262_18	1800001	1910000
AE017262_19	1900001	2010000
AE017262_20	2000001	2110000
AE017262_21	2100001	2210000
AE017262_22	2200001	2310000
AE017262_23	2300001	2410000
AE017262_24	2400001	2510000
AE017262_25	2500001	2610000
AE017262_26	2600001	2710000
AE017262_27	2700001	2810000
AE017262_28	2800001	2905187

Continuation (29 of 29) of AE017262 from base 2800001 (AE017262 Listeria monocytogenes)

Query Match 83.2%; Score 2197.6; DB 15; Length 105187;
Best Local Similarity 88.1%; Pred. No. 0;
Matches 2511; Conservative 0; Mismatches 114; Indels 225; Gaps 2;

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QY 1 TAAACCGCGGTATTAATAATGATTATAGAACCGAATAGGAGTCGCGCAAAATTCGAAAAC 60
Db 67562 TAAACCGCGGTATTAATAATGATTATAGAAAACGAATAGGAGTCGCGCAAAATTCGAAAAC 67621
QY 61 TACTAAATAGTAAATGCTCATTAGTTTAAACCATGTTTCAAAACCGCTTTTAAAC 120
Db 67622 TTCTAAATAATTAATAGCTTCATTAGTTTAAACCTGGTTTCAAAACCCCAATTTTAAAC 67681
QY 121 ATTCGCAACCAAGATGATGTTTATGTATAATACGACAGAAATCACTACTGATAAGAAAC 180
Db 67682 ATTCGCAACCAAGATGATGTTGATTGATTAGTACGACAGAAATCACTACTGATAAGAAAT 67741
QY 181 AAGCTCAACTCAACCAACTATAAAAAACACACTCAAGCCGCTCAAAACAAAGTTTTAA 240
Db 67742 AAGCTCAACTCAACCAACTATAAAAAACCACTCAAGCTGGTCAAAACAAAGTTTTAA 67801
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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 14, 2006, 13:20:45 ; Search time 125.513 Seconds
(without alignments)
10189.779 Million cell updates/sec

Title: US-10-767-441-27

Perfect score: 20

Sequence: 1 ttacggctggattgtctgtg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*
1: gb_env.*
2: gb_pat.*
3: gb_ph.*
4: gb_pl.*
5: gb_pr.*
6: gb_ro.*
7: gb_ats.*
8: gb_sy.*
9: gb_un.*
10: gb_vi.*
11: gb_ov.*
12: gb_htg.*
13: gb_in.*
14: gb_om.*
15: gb_ba.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	2556	2 AX413703	AX413703 Sequence
C 2	20	100.0	2556	2 AX415879	AX415879 Sequence
C 3	20	100.0	105187	15 AE017262_28	Continuation (29 o
C 4	20	100.0	225528	15 AL591984	AL591984 Listeria
C 5	20	100.0	244528	2 AX641673	AX641673 Sequence
C 6	19	95.0	125366	11 BX649277	BX649277 Zebrafish
C 7	19	95.0	165089	11 BX649385	BX649385 Zebrafish
C 8	19	95.0	222879	11 BX324175	BX324175 Zebrafish
C 9	19	95.0	263011	12 BX914199	BX914199 Danio rer
C 10	17.4	87.0	189351	12 AC156120	AC156120 Bos tauru
C 11	17.4	87.0	189351	12 AC156120	AC156120 Bos tauru
C 12	17.4	87.0	194849	12 AC147015	AC147015 Zea mays
C 13	17.4	87.0	238338	12 AC162356	AC162356 Bos tauru
C 14	17	85.0	110000	15 AE000512_13	Continuation (14 o
C 15	17	85.0	311522	12 AC162513	AC162513 Bos tauru
C 16	16.8	84.0	183	7 AF235312	AF235312 Sus scrof
C 17	16.8	84.0	1458	4 AF247136	AF247136 Capsicum
C 18	16.8	84.0	89384	12 AP007333	AP007333 Lotus cor

C 19	16.8	84.0	110000	4 AP007171_04	Continuation (5 of
C 20	16.8	84.0	110000	15 AP006627_29	Continuation (30 o
C 21	16.8	84.0	110000	15 BX950851_48	Continuation (49 o
C 22	16.8	84.0	112732	5 AL160007	AL160007 Human DNA
C 23	16.8	84.0	113949	12 AC170863	AC170863 Mus muscu
C 24	16.8	84.0	143794	5 AC009315	AC009315 Homo sapi
C 25	16.8	84.0	148055	12 AC128178	AC128178 Rattus no
C 26	16.8	84.0	167417	12 AC151166	AC151166 Bos tauru
C 27	16.8	84.0	179038	12 AC171229	AC171229 Bos tauru
C 28	16.8	84.0	182371	12 AC175370	AC175370 Cavia por
C 29	16.8	84.0	185573	12 AC173137	AC173137 Bos tauru
C 30	16.8	84.0	186522	12 AC169050	AC169050 Bos tauru
C 31	16.8	84.0	194074	5 AC090095	AC090095 Homo sapi
C 32	16.8	84.0	195446	6 AC133967	AC133967 Mus muscu
C 33	16.8	84.0	195714	6 AC159208	AC159208 Mus muscu
C 34	16.8	84.0	199810	5 AC018443	AC018443 Homo sapi
C 35	16.8	84.0	208603	6 AC135567	AC135567 Mus muscu
C 36	16.8	84.0	211158	6 AC123658	AC123658 Mus muscu
C 37	16.8	84.0	222568	12 AC128034	AC128034 Rattus no
C 38	16.8	84.0	231406	12 AC132626	AC132626 Rattus no
C 39	16.8	84.0	238608	12 AC095637	AC095637 Rattus no
C 40	16.8	84.0	243299	12 AC129672	AC129672 Rattus no
C 41	16.8	84.0	245536	6 AC093320	AC093320 Mus muscu
C 42	16.8	84.0	250502	12 AC098191	AC098191 Rattus no
C 43	16.8	84.0	253762	12 AC094601	AC094601 Rattus no
C 44	16.8	84.0	265323	12 AC095987	AC095987 Rattus no
C 45	16.8	84.0	269126	12 AC096191	AC096191 Rattus no

ALIGNMENTS

RESULT 1	AX413703	Sequence 694 from Patent WO0228891.	2556 bp	DNA	linear	PAT 02-SEP-2002
LOCUS	AX413703	AX413703				
DEFINITION	AX413703	AX413703				
ACCESSION	AX413703	AX413703				
VERSION	AX413703.1	GI:21446160				
KEYWORDS						
SOURCE		Listeria monocytogenes EGD-e				
ORGANISM		Listeria monocytogenes EGD-e				
REFERENCE		1				
AUTHORS		Kunst, F. and Glaser, P.				
TITLE		Listeria inocua, genome and applications				
JOURNAL		Patent: WO 0228891-A 694 11-APR-2002;				
		INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE				
		SCIENTIFIQUE (CNRS) (FR)				
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Source		1..2556				
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		/mol_type="unassigned DNA"				
		/db_xref="taxon:169963"				

ORIGIN						
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Best Local Similarity		100.0%;	Pred No. 1.8;			
Matches	20;	Conservative	0;	Mismatches	0;	Gaps 0;
Indels						
QY	1	TTACGGCTGGATTGTCTGTG 20				
Db	1447	TTACGGCTGGATTGTCTGTG 1428				
RESULT 2						
AX415879/c						
LOCUS	AX415879	Sequence 2870 from Patent WO0228891.	2556 bp	DNA	linear	PAT 02-SEP-2002
DEFINITION	AX415879	AX415879				
ACCESSION	AX415879	AX415879				
VERSION	AX415879.1	GI:21448336				
KEYWORDS						
SOURCE		Listeria monocytogenes EGD-e				
ORGANISM		Listeria monocytogenes EGD-e				

Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE

1 Kunat, F. and Glaser, P.
Listeria innocua, genome and applications
Patent: WO 0228891-A 2870 11-APR-2002;
INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE (CNRS) (FR)

FEATURES

source
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Location/Qualifiers
/organism="Listeria monocytogenes EGD-e"
/mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 20; DB 2; Length 2556;

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACGGCTGGATTGCTGTG 20

DB 1447 TTACGGCTGGATTGCTGTG 1428

RESULT 3

AE017262_28/c

WPCOMMENT

Sequence split into 29 fragments LOCUS AE017262 Accession AE017262

Fragment Name Begin End

AE017262_00 1 110000

AE017262_01 100001 210000

AE017262_02 200001 310000

AE017262_03 300001 410000

AE017262_04 400001 510000

AE017262_05 500001 610000

AE017262_06 600001 710000

AE017262_07 700001 810000

AE017262_08 800001 910000

AE017262_09 900001 1010000

AE017262_10 1000001 1110000

AE017262_11 1100001 1210000

AE017262_12 1200001 1310000

AE017262_13 1300001 1410000

AE017262_14 1400001 1510000

AE017262_15 1500001 1610000

AE017262_16 1600001 1710000

AE017262_17 1700001 1810000

AE017262_18 1800001 1910000

AE017262_19 1900001 2010000

AE017262_20 2000001 2110000

AE017262_21 2100001 2210000

AE017262_22 2200001 2310000

AE017262_23 2300001 2410000

AE017262_24 2400001 2510000

AE017262_25 2500001 2610000

AE017262_26 2600001 2710000

AE017262_27 2700001 2810000

AE017262_28 2800001 2905187

Continuation (29 of 29) of AE017262 from base 2800001 (AE017262 Listeria monocytogenes s

Query Match 100.0%; Score 20; DB 15; Length 105187;

Best Local Similarity 100.0%; Pred. No. 2.1;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACGGCTGGATTGCTGTG 20

DB 69060 TTACGGCTGGATTGCTGTG 69041

RESULT 4

AL591984/c

LOCUS

DEFINITION

AL591984 Listeria monocytogenes strain EGD, complete genome, segment 12/12.

AL591984 AL591824

VERSION

AL591984.1 GI:16412145

KEYWORDS

Listeria monocytogenes

SOURCE

Listeria monocytogenes

ORGANISM

Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE

1

AUTHORS

Glaser, P., Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A.,

Baquero, F., Berche, P., Bloeker, H., Brandt, P., Chakraborty, T.,

Charbit, A., Chetoui, F., Couve, E., de Daruvar, A., Denoux, P.,

Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L.,

Dussurget, O., Entian, K.D., Fsihi, H., Garcia-del Portillo, F.,

Garrido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T.,

Kauf, J., Jackson, D., Jones, L.M., Kaerst, U., Knecht, J., Kuhn, M.,

Kunst, F., Kurapkat, G., Madueno, E., Maitournam, A., Vicente, J.M.,

Ng, E., Nedjari, H., Nordsiek, G., Novella, S., de Pablo, B.,

Perez-Diaz, J.C., Purcell, R., Remmel, B., Rose, M., Schlueter, T.,

Simoes, N., Tierrez, A., Vazquez-Boland, J.A., Voss, H., Wehland, J. and

Cossart, P.

TITLE

Comparative genomics of Listeria species

JOURNAL

Science 294 (5543), 849-852 (2001)

PUBMED

11679669

REFERENCE

2 (bases 1 to 225528)

AUTHORS

Glaser, P., Frangeul, L. and Rusniok, C.

TITLE

Direct Submission

JOURNAL

Submitted (06-JUN-2001) Glaser P., Institut Pasteur, Genomique des

Microorganismes Pathogenes, 25 rue du Docteur Roux, 75724 Paris

Cedex 15, FRANCE

E-mail: pglaser@pasteur.fr

Phone: +33 1 45 68 89 96, Fax: +33 (0)1 45 68 87 86.

FEATURES

Location/Qualifiers

1. 225528

/organism="Listeria monocytogenes"

/mol_type="genomic DNA"

/strain="EGD-e"

/db_xref="taxon:1639"

complement (56. .775)

/gene="lmo2646"

complement (56. .775)

/gene="lmo2646"

/codon_start=1

/transl_table=1

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/db_xref="GI:16412146"

/db_xref="InterPro:IPR010763"

/db_xref="UniProtKB/TREMBL:Q8Y429"

/translation="MNKKKFNLPKNNFALFNFLAKNSLEVMVAARGFAVPGIV

ATNYETAEEANVVKELQTTAEVISGLGGGQWQNRDVLHFLAPNSHINQIET

AGLTLGLLPETYTNALVRPTGKVGIVKLSGDEITAEBAVDYCLSANIPSIKFMSEIG

TKYLDELVLTAKIADKGIYGIIEPAGGIGADNILEITTAIKSTGIPFYMPIFGKTI

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complement (64. .69)

/gene="lmo2645"

complement (64. .69)

/gene="lmo2645"

complement (join(735. .1484,1493. .1498))

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complement (735. .1484)

/gene="lmo2647"

/note="similar to creatinine amidohydrolase"

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/transl_table=1

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/translation="MLYADENSFDIGAKITTKPVLIPFGIAVEAHGPHLPGLTDNILA

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LFVPVSGHLGNMAALKDAARELYAKFDPVILHIFYPNIQKLANVRESGKANHVTYIH

ACEITSLMLYLSPEMDMSRAIDDPDLPIDADFTPTPWQTFKTAIVGEATLATAE

KGEYLIETLTKTCVELIKLEQEKIRKSTEME"

complement (785. .790)

/gene="lmo2646"

complement (785. .790)

Dehous, P., Dussurget, O., Chetouani, F., Nedjari, H., Glaser, P., Kunst, F., Cosart, P., Daniels, J., Goebel, W., Krefit, J., Kuhn, M., Ng, E., Vasquez-Boland, J., Dominguez-Bernal, G., Garrido-Garcia, P., Tierrez-Martinez, A., Amend, A., Chakraborty, T., Domann, E., Hain, T., Berche, P., Charbit, A., Durand, L., Perez-Diaz, J. C., Baquero, F., Garcia del Portillo, F., Gomez-Lopez, N., Maduenio, E., de Pablo, B., Wehland, J., Kaerst, U., Entian, K. D., Hauf, J., Rose, M. and Voss, H. *Listeria monocytogenes* genome, polypeptides and uses Patent: WO 01/118-A 2863 11-APR-2001; INSTITUT PASTEUR (FR)

TITLE JOURNAL

FEATURES

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1. 244528
/organism="Listeria monocytogenes"
/mol_type="unassigned DNA"
/db_xref="taxon:1639"
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0.349.980 length: 349.980 <223>seq 2855 : From 0.300.001
to 0.649.980 length: 349.980 <223>seq 2856 : From
0.600.001 to 0.949.980 length: 349.980 <223>seq 2857 :
From 0.900.001 to 1.249.980 length: 349.980 <223>seq 2858
: From 1.200.001 to 1.549.980 length: 349.980 <223>seq
2859 : From 1.500.001 to 1.849.980 length: 349.980
<223>seq 2860 : From 1.800.001 to 2.149.980 length:
349.980 <223>seq 2861 : From 2.100.001 to 2.449.980
length: 349.980 <223>seq 2862 : From 2.400.001 to
2.749.980 length: 349.980 <223>seq 2863 : From 2.700.001
to 2.944.528 length: 244.528"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACGGCTGGATTGCTGTG 20
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Db 208599 TTACGGCTGGATTGCTGTG 208580

RESULT 6
BX649277/c 125366 bp DNA linear VRT 23-OCT-2003
LOCUS
DEFINITION
Zebrafish DNA sequence from clone DKEYP-67A10 in linkage group 20,
complete sequence.

ACCESSION
BX649277 GI:37936349
VERSION
KEYWORDS
HTG.

SOURCE
Danio rerio (zebrafish)
ORGANISM
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

REFERENCE
1 (bases 1 to 125366)

AUTHORS
Lovell, J.
Direct Submission
Submitted (22-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Oct 23, 2003 this sequence version replaced gi:37718596.

COMMENT

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhiyong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml DKEYP-67A10 is from a Zebrafish BAC library VECTOR: pindigobAC-5.

FEATURES

Location/Qualifiers
1. 125366
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/clones="DKEYP-67A10"
/clone_lib="DanioKeyPilot"

ORIGIN

Query Match 95.0%; Score 19; DB 11; Length 125366;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TTACGGCTGGATTGCTGT 19
|||||
Db 123540 TTACGGCTGGATTGCTGT 123522

RESULT 7

LOCUS
BX649385 165089 bp DNA linear VRT 28-OCT-2003
DEFINITION
Zebrafish DNA sequence from clone CH211-127M24 in linkage group 20,
complete sequence.

ACCESSION
BX649385
VERSION
BX649385.8 GI:38044030
KEYWORDS
HTG.

SOURCE

ORGANISM
Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 165089)

Dyer, L.

Direct Submission

Submitted (28-OCT-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Oct 29, 2003 this sequence version replaced gi:37992151.

COMMENT

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C	1	21	100.0	759	2	AX415918 Sequence
	2	21	100.0	2556	2	AX413703 Sequence
	3	21	100.0	2556	2	AX415879 Sequence
	4	21	100.0	105187	15	Continuation (29.6)
	5	21	100.0	225528	15	AX591984 Listeria
	6	21	100.0	244528	2	AX641673 Sequence
	7	18.4	87.6	265444	12	AC132999 Rattus n
	8	17.8	84.8	419	2	AC132999 Rattus n
	9	17.8	84.8	1310	5	BC20914 Sequence
	10	17.8	84.8	2017	4	BC065197 Homo sapi
C	11	17.8	84.8	3084	2	AX4101759 Homo sapi
	12	17.8	84.8	110000	4	AX416693 Sequence
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	14	17.8	84.8	209060	5	AP003239 Oryza sat
	15	17.4	82.9	155656	5	AC010733 Homo sapi
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	17	16.8	80.0	92466	5	AC092114 Homo sapi
	18	16.8	80.0	106123	5	AL158015 Human DNA
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	20	16.8	80.0	106123	5	AL158015 Human DNA

Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE 1
 AUTHORS Kunst, F. and Glaser, P.
 TITLE Listeria innocua, genome and applications
 JOURNAL Patent: WO 0228891-A 694 11-APR-2002;
 INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
 SCIENTIFIQUE (CNRS) (FR)

FEATURES
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ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 2556;

Best Local Similarity 100.0%; Pred. No. 1.4;
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QY 1 TGTAAACCCGCTTACACAGTT 21

DB 837 TGTAAACCCGCTTACACAGTT 857

RESULT 3

AX415879 AX415879 2556 bp DNA linear PAT 02-SEP-2002
 LOCUS
 DEFINITION Sequence 2870 from Patent WO0228891.
 ACCESSION AX415879
 VERSION AX415879.1 GI:21448336

KEYWORDS Listeria monocytogenes EGD-e
 SOURCE Listeria monocytogenes EGD-e
 ORGANISM Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE 1

Kunst, F. and Glaser, P.
 TITLE Listeria innocua, genome and applications
 JOURNAL Patent: WO 0228891-A 2870 11-APR-2002;
 INSTITUT PASTEUR (FR) ; CENTRE NATIONAL DE LA RECHERCHE
 SCIENTIFIQUE (CNRS) (FR)

FEATURES
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 /mol_type="unassigned DNA"
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ORIGIN

Query Match 100.0%; Score 21; DB 2; Length 2556;

Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACCCGCTTACACAGTT 21

DB 837 TGTAAACCCGCTTACACAGTT 857

RESULT 4

AX417262_28
 WPCOMMENT
 Sequence split into 29 fragments LOCUS AE017262 Accession AE017262

Fragment Name	Begin	End
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AE017262_01	100001	210000
AE017262_02	200001	310000
AE017262_03	300001	410000
AE017262_04	400001	510000
AE017262_05	500001	610000
AE017262_06	600001	710000
AE017262_07	700001	810000
AE017262_08	800001	910000
AE017262_09	900001	1010000
AE017262_10	1000001	1110000
AE017262_11	1100001	1210000
AE017262_12	1200001	1310000

AE017262_13 1300001 1410000
 AE017262_14 1400001 1510000
 AE017262_15 1500001 1610000
 AE017262_16 1600001 1710000
 AE017262_17 1700001 1810000
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 AE017262_20 2000001 2110000
 AE017262_21 2100001 2210000
 AE017262_22 2200001 2310000
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 AE017262_27 2700001 2810000
 AE017262_28 2800001 2905187

Continuation (29 of 29) of AE017262 from base 2800001 (AE017262 Listeria monocytogenes
 Query Match 100.0%; Score 21; DB 15; Length 105187;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 68450 TGTAAACCCGCTTACACAGTT 68470

RESULT 5

AL591984 AL591984 225528 bp DNA linear BCT 16-APR-2005
 LOCUS
 DEFINITION Listeria monocytogenes strain EGD, complete genome, segment 12/12.
 ACCESSION AL591984 AL591824

VERSION AL591984.1 GI:16412145
 KEYWORDS Listeria monocytogenes
 SOURCE Listeria monocytogenes
 ORGANISM Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.

REFERENCE 1

Glaser, P., Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A.,
 Baquero, F., Berche, P., Bloeker, H., Brandt, P., Chakraborty, T.,
 Charbit, A., Chetouani, F., Couve, E., de Daruvar, A., Dehoux, P.,
 Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L.,
 Dussurget, O., Ertan, K. D., Fsihi, H., Garcia-del Portillo, P.,
 Garrido, P., Gautier, L., Goebel, W., Gomez-Lopez, N., Hain, T.,
 Haut, J., Jackson, D., Jones, L. M., Kaerst, U., Kretz, J., Kuhn, M.,
 Kunst, F., Kurapkat, G., Madueno, E., Maitournam, A., Vicente, J. M.,
 Ng, E., Nedjari, H., Nordsiek, G., Novella, S., de Pablo, B.,
 Perez-Diaz, J. C., Purcell, R., Remmel, B., Rose, M., Schlueter, T.,
 Simoes, N., Tierrez, A., Vazquez-Boland, J. A., Voss, H., Wehland, J. and
 Cossart, P.

TITLE Comparative genomics of Listeria species
 JOURNAL Science 294 (5543), 849-852 (2001)

PUBMED 11679669

REFERENCE 2 (bases 1 to 225528)

Glaser, P., Frangeul, L. and Rusniok, C.

AUTHORS

TITLE

JOURNAL

COMMENT

Phone: +33 1 45 68 89 96; Fax: +33 (0) 1 45 68 87 86.

FEATURES

source

1. .225528

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